IN THE CLAIMS:

Please cancel claims 1, 4, and 6 without prejudice to their later prosecution.

Please amend the following claims.

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2. (Amended) The probe of claim [1] 15, wherein said probe is complementary to rRNA or rDNA.

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(Amended) A nucleic acid hybrid formed between a nucleotide polymer of claim [6] 19 and a [nucleic acid] nucleotide [sequence] polymer complementary thereto.

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11. (Amended) A nucleic acid hybrid formed between an oligonucleotide consisting essentially of a member of the group consisting of the oligonucleotides of the sequences CCCCTTTTAAATTACTAACATGCG, GCACCAGTTCTCAGCGTTC, and CCATTAGTTAGTGGGTTCC [and the oligonucleotides complementary thereto], and a [nucleic acid sequence] nucleotide polymer [substantially] sufficiently complementary thereto to allow hybridization under stringent hybridization conditions.

12. (Amended) A probe mix [comprising the polymers of claims 8, 9, and 10] consisting essentially of at least two of

the sequences CCCCTTTTAAATTACTAACATGCG, GCACCAGTTCTCAGCGTTC, and CCATTAGTTAGTGGGTTCC, or a probe mix consisting essentially of Oligonucleotides complementary thereto.

13. (Amended) A probe mix [comprising the polymer of claims 8, 9, or 10] consisting essentially of at least two of the sequences CCCCTTTTAAATTACTAACATGCG, GCACCAGTTCTCAGCGTTC, or CCATTAGTTGGGGTTCC, or a probe mix consisting essentially of oligonucleotides complementary thereto, and a helper probe.

14. (Amended) The probe mix of claim 13 wherein said helper probe is chosen from [an] oligonucleotides [having] comprising the sequence CAACGCAGGTCCATCTCATAGTGGAGCAATTG, TTAGTCTCTTATGCGGTATTAGCTATCGTTTCC, CAACTCCTTGAACCGGTGCAA, TACTTGCATGTATTAGGCACGCCGCC, CACTGCGTCTTCCTTCATAACCTTAACAGTTATGGA [and] or

CACTGCGTCTTCCTTCATAACCTTAACAGTTATGGA [and] or

Please add the following new claims.

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probe having sufficient complementarity to the rRNA or rDNA sequences of <u>Streptococcus pyogenes</u>, or to sequences complementary thereto, to distinguish, under hybridization

conditions, Streptococcus pyogenes from Streptococcus anginosus, Streptococcus constellatus, Streptococcus dysgalactiae, Streptococcus equinus, Streptococcus mitis, Streptococcus morbillorum, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus salivarius, Streptococcus sanguis, Streptococcus uberis, Streptococcus species Group C, Streptococcus species Group F2, Streptococcus species Group G, Streptococcus species Group C, Streptococcus species Group C

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- 16. (New) The probe of claim 15, wherein said probe distinguishes <u>Streptococcus</u> pyogenes from all other <u>Streptococcus</u> species.
- 17. (New) The hybridization assay probe of claim 15, wherein said probe consists essentially of an oligonucleotide having sufficient complementarity to a region of ribosomal nucleic acid which varies between species of Streptococci to hybridize to Streptococcus species.
- 18. (New) An oligonucleotide hybridization assay probe mix which distinguishes <u>Streptococcus pyogenes</u> and <u>Streptococcus "equi"</u> (CDC) from <u>Streptococcus anginosus</u>, <u>Streptococcus constellatus</u>, <u>Streptococcus dysgalactiae</u>,

Streptococcus equinus, Streptococcus mitis, Streptococcus
morbillorum, Streptococcus mutans, Streptococcus pneumoniae,
Streptococcus salivarius, Streptococcus sanguis, Streptococcus
uberis, Streptococcus species Group C, Streptococcus species
Group F2, Streptococcus species Group G, Streptococcus species
Group C, and Streptococcus equi.

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of between 10 and 10 nucleotides, inclusive, able to form a hybrid in 0.1 M lithium succinate buffer containing 10% lithium lauryl sulfate at 60°C with a nucleotide polymer having a nucleotide base sequence selecting from a group consisting of 5' CCCCTTTAAATTACTAACATGCG, 5' CGCATGTTAGTAATTTAAAAGGGG,

- *ν*/
- 3' GGGGAAAAUUUAAUGAYUGUACGC, 3' GCGUACAAUCAUUAAAUUUUCCCC,
- 5' GCACCAGTTCTCAGGGTTC, 5' GAACGCTGAGAACTGGTGC,
- 3' CGUGGUCAAGAGU¢GCAAG, 3' CUUGCGACUCUUGACCACG,
- 5' CCATTAGTTAGTGGGTTCC, 5'GGAACCCACTAACTAATGG,
- 3' GGUAAUCAAUCACCCAAGG and 3' CCUUGGGUGAUUGAUUACC.

20. (New) The oligonucleotide of claim 19, wherein said oligonucleotide consists essentially of between 15 to 100 bases.

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((New) The oligonucleotide of claim 18, wherein said oligonucleotide consists essentially of between 10-50 bases.

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22. (New) The oligonucleotide of claim 18, wherein said oligonucleotide consists essentially of between 20-50 bases.

pyogenes from Streptococcus anginosus, Streptococcus
constellatus, Streptococcus dysgalactiae, Streptococcus equinus,
Streptococcus mitis, Streptococcus morbillorum, Streptococcus
mutans, Streptococcus pneumoniae, Streptococcus salivarius,
Streptococcus sanguis, Streptococcus uberis, Streptococcus
species Group C, Streptococcus species Group F2, Streptococcus
species Group G, Streptococcus species Group C, Streptococcus
"equi", and Streptococcus equi, comprising the step of
hybridizing a nucleic acid hybridization assay probe which is
able to hybridize to Streptococcus species.

REMARKS

The invention concerns nucleic acid probes which are able to distinguish Streptococcus.

Streptococcus.

The specification has been amended as requested by the Examiner to meet the Examiner's objections. In order to clarify